### SEQUENCE LISTING

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<110> Schlauder, George G
      Erker, James C
      Desai, Suresh M
      Dawson, George J
      Mushawar, Isa K
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tac cct aaa atc cag acc acg agc cgt gtg cta cgg tcc ctg ttt t Tyr Pro Lys Ile Gln Thr Thr Ser Arg Val Leu Arg Ser Leu Phe 1 1105 1110 1115	
aat gaa ccg gcc att ggc cag aag ttg gtt ytc acg cag gcg gca a Asn Glu Pro Ala Ile Gly Gln Lys Leu Val Xaa Thr Gln Ala Ala I 1125 1130 1135	
gct gct aac cct ggt gcg att acg gtc cac gaa gct cag ggt gcc a	acc 3456

Ala Ala Asn Pro 1140	Gly Ala Ile :	Thr Val His Glu 1145	Ala Gln Gly Ala Thr 1150	
	Thr Ile Ile		gcc agg ggc ctt atc Ala Arg Gly Leu Ile 1165	3504
		Ile Val Ala Leu	act cgc cac act gag Thr Arg His Thr Glu 1180	3552
			cgt gag gtc ggc att Arg Glu Val Gly Ile 1200	3600
Ser Asp Val Ile	-		ggt ggc gag gtc ggc Gly Gly Glu Val Gly 1215	3648
_			cct gat caa aac ctc Pro Asp Gln Asn Leu 1230	3696
	Ala Phe Pro I	-	att agt gct tac cat Ile Ser Ala Tyr His 1245	3744
		His Arg Pro Ala	cct gtc gcc gcc gtc Pro Val Ala Ala Val 1260	3792
			ctc tac atg cca cag Leu Tyr Met Pro Gln 1280	3840
Glu Leu Thr Val			gag ctt acg gat ata Glu Leu Thr Asp Ile 1295	3888
	Met Ala Ala E	ro Ser Gln Arg	aag gct gtt ctc tca Lys Ala Val Leu Ser 1310	3936
	Arg Tyr Gly A		cta tat gag gcg gcg Leu Tyr Glu Ala Ala 1325	3984
• •		eu Ala Arg Phe	atc cct act atc ggg Ile Pro Thr Ile Gly 1340	4032
cct gtt cag gct Pro Val Gln Ala 1345	acc aca tgt g		ttg gtt gag gct atg	4080
	Thr Thr Cys G	1355	1360	

136	5	1370	1375
aat cgt gat gtc tc Asn Arg Asp Val Se 1380		Phe Gln Lys Xaa C	ys Asn Lys
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tcg gcc tgg agt aag Ser Ala Trp Ser Lys 1410			
gcc att gaa aaa gaa Ala Ile Glu Lys Glu 1425			
ggc gac gct tat gag Gly Asp Ala Tyr Glu 144	ı Glu Ser Val Phe		
ggg tca tgt atg gta Gly Ser Cys Met Val 1460		Phe Ser Glu Phe As	sp Ser Thr
cag aat aat ttc tc Gln Asn Asn Phe Sen 1475			
ggc atg cct caa tgg Gly Met Pro Gln Trp 1490 ,			_
tgg att ctg cag gcg Trp Ile Leu Gln Ala 1505			
cat tet ggt gag cet His Ser Gly Glu Pro 1525	Gly Thr Leu Leu		
gcg att ata gca cat Ala Ile Ile Ala His 1540			al Ala Ala
ttt aag ggt gat gat Phe Lys Gly Asp Asp 1555	<del>-</del>		
cgc aat gca gct gcc Arg Asn Ala Ala Ala 1570			
gat tac cgc cct ato Asp Tyr Arg Pro Ile 1585			

	4848
aag aat tgg ggc ccc ggc ccg gaa cgt gct gag cag ctg cgt ctt gct Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala 1620 1625 1630	4896
gtc tgc gac ttc ctt cga ggg ttg acg aat gtt gcg cag gtc tgt gtt Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala Gln Val Cys Val 1635 1640 1645	4944
gat gtt gtg tcc cgt gtc tat gga gtc agc ccc ggg ctc gta cat aac Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly Leu Val His Asn 1650 1655 1660	4992
ctt att ggc atg ctg cag acc atc gcc gat ggc aag gcc cac ttt aca Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys Ala His Phe Thr 1665 1670 1675 1680	5040
gag act att aaa cct gta ctt gat ctc aca aat tcc atc ata cag cgg Glu Thr Ile Lys Pro Val Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg 1685 1690 1695	5088
gtg gaa tga ataacatgtc ttttgcatcg cccatgggat cacc atg cgc cct agg Val Glu Met Arg Pro Arg 1700	5143
gct gtt ctg ttg ttg ttc ctc atg ttt ctg cct atg ctg ccc gcg cca Ala Val Leu Leu Phe Leu Met Phe Leu Pro Met Leu Pro Ala Pro 1705 1710 1715	5191
ccg gcc ggt cag ccg tct ggc cgt cgc cgt ggg cgc agc ggc ggt Pro Ala Gly Gln Pro Ser Gly Arg Arg Gly Arg Arg Ser Gly Gly 1720 1725 1730 1735	5239
Pro Ala Gly Gln Pro Ser Gly Arg Arg Gly Arg Arg Ser Gly Gly 1720 1725 1730 1735	5239 5287
Pro Ala Gly Gln Pro Ser Gly Arg Arg Gly Arg Arg Ser Gly Gly 1720 1725 1730 1735  gcc ggc ggt ggt ttc tgg agt gac agg gtt gat tct cag ccc ttc gcc Ala Gly Gly Gly Phe Trp Ser Asp Arg Val Asp Ser Gln Pro Phe Ala 1740 1745 1750	
Pro Ala Gly Gln Pro Ser Gly Arg Arg Gly Arg Arg Ser Gly Gly 1720 1725 1730 1735  gcc ggc ggt ggt ttc tgg agt gac agg gtt gat tct cag ccc ttc gcc Ala Gly Gly Gly Phe Trp Ser Asp Arg Val Asp Ser Gln Pro Phe Ala 1740 1745 1750  ctc ccc tat att cat cca acc aac ccc ttc gcc gcc gat gtc gtt tca Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser 1755 1760 1765	5287
Pro Ala Gly Gln Pro Ser Gly Arg Arg Gly Arg Arg Ser Gly Gly 1720 1725 1730 1735  gcc ggc ggt ggt ttc tgg agt gac agg gtt gat tct cag ccc ttc gcc Ala Gly Gly Phe Trp Ser Asp Arg Val Asp Ser Gln Pro Phe Ala 1740 1745 1750  ctc ccc tat att cat cca acc aac ccc ttc gcc gcc gat gtc gtt tca Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser 1755 1760 1765  caa ccc ggg gct gga act cgc cct cga cag ccg ccc cgc ccc ctc ggt Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly 1770 1775 1780	5287 5335

cct gat aca gct cct gta cct gat gtt gac Pro Asp Thr Ala Pro Val Pro Asp Val Asp 1820 1825	
cgc cgg cag tac aat ttg tct acg tcc ccg Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro 1835 1840	
tct ggt act aat ctg gtt ctc tat gct gcc Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala 1850 1855	
cct ctt cag gat ggc acc aac act cat att Pro Leu Gln Asp Gly Thr Asn Thr His Ile: 1865 1870	
	Thr Ile Arg Tyr Arg Pro 890 1895
ttg gtg cca aat gct gtt ggt ggt tat gct Leu Val Pro Asn Ala Val Gly Gly Tyr Ala 1900 1905	
cct caa act aca act acc cct act tct gtt Pro Gln Thr Thr Thr Thr Pro Thr Ser Val 1915 1920	<del>-</del>
tet act gat gte agg ate ttg gte eag eee ser Thr Asp Val Arg Ile Leu Val Gln Pro	
gtc atc cct agt gaa cgc ctt cac tac cgc val Ile Pro Ser Glu Arg Leu His Tyr Arg 1945	
gtt gag acc acg ggt gtg gcc gaa gag gag Val Glu Thr Thr Gly Val Ala Glu Glu Glu 1960 1965 1	
atg ctt tgt att cat ggc tcc cct gtt aac Met Leu Cys Ile His Gly Ser Pro Val Asn 1980 1985	Ser Tyr Thr Asn Thr Pro
tac acc ggt gca ttg ggg ctt ctt gat ttt g Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe 2 1995 2000	
aga aat ttg aca ccc ggg aac act aac acc arg Asn Leu Thr Pro Gly Asn Thr Asn Thr 2010 2015	
agc aca gcc cgc cac cgg ctg cgc cgc ggt c Ser Thr Ala Arg His Arg Leu Arg Arg Gly 2 2025 2030	
ctc acc acc aca gca gcc aca cgc ttc atg	aag gat ttg cat ttt act 6199

Leu Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu His Phe Thr 2040 2045 2050 2055	
ggt acg aac ggc gtt ggt gag gtg ggt cgt ggt att gcc ctg act ctg Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala Leu Thr Leu 2060 2065 2070	6247
ttt aat ctt gct gat acg ctt ctt ggt ggt tta ccg aca gaa ttg att Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile 2075 2080 2085	6295
tcg tcg gct ggg ggt caa ctg ttt tac tcc cgc cct gtt gtc tcg gcc Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala 2090 2095 2100	6343
aat ggc gag cca aca gta aag tta tac aca tct gtt gag aat gcg cag Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln 2105 2110 2115	6391
caa gac aag ggc atc acc att cca cac gac ata gat tta ggt gac tcc Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp Leu Gly Asp Ser 2120 2125 2130 2135	6439
cgt gtg gtt atc cag gat tat gat aac cag cac gaa caa gat cga cct Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln Asp Arg Pro 2140 2145 2150	6487
acc ccg tca cct gcc ccc tcc cgc cct ttc tca gtt ctt cgt gcc aat Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu Arg Ala Asn 2155 2160 2165	6535
gat gtt ttg tgg ctc tct ctc act gcc gct gag tac grc cag acc acg Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Xaa Gln Thr Thr 2170 2175 2180	6583
tat ggg tcg tcc acc aac cct atg tat gtc tct gat aca gtc acg ctt Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr Val Thr Leu 2185 2190 2195	6631
gtt aat gta gcc act ggt gct cag gct gtt gcc cgc tct ctt gac tgg Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg Ser Leu Asp Trp 2200 2205 2210 2215	6679
tct aaa gtt act ctg gat ggt cgc cct ctt act acc att cag cag tat Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr Ile Gln Gln Tyr 2220 2225 2230	6727
tct aag aaa ttt tat gtt ctc ccg ctt cgs ggg aag ctg tcc ttt tgg Ser Lys Lys Phe Tyr Val Leu Pro Leu Xaa Gly Lys Leu Ser Phe Trp 2235 2240 2245	6775
gag gct ggt acg acc aag gcc ggc tac ccg tat aat tat aat acc act Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr 2250 2255 2260	6823
gct agt gac caa att ttg att gag aac gcg gcc ggt cac cgt gtc gcc Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His Arg Val Ala	6871

2265	2270	2275		
		ggt gcc ggc cct acc Gly Ala Gly Pro Thr 2290		919
Ala Val Gly Val	·-·	tcg gcc ctt gct gtt Ser Ala Leu Ala Val 2305		967
	Pro Ala Arg Ala I	cat act ttt gat gat His Thr Phe Asp Asp 320		015
		ggt tgt gca ttc caa Gly Cys Ala Phe Gln 2340	Ser Thr Ile	063
		aag gta ggt aaa acc Lys Val Gly Lys Thr 2355		111
taa ttaattcctt	tgtgccccc ttcgcag	gttc tctttggctt tat	ttctcat 7	164
2360				
ttctgctttc cgcg	ctccct ggaaaaaaaa	aaaaaaa	7	202
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<211> 1698 <212> PRT <213> Hepatitis <400> 91 Pro Gly Ile Thr	Thr Ala Ile Glu (5) Asn Ala Val Val Val Val Leu Ile Asn Leu M	10 Val Arg Pro Phe Leu 25 Met Gln Pro Arg Gln	Ser Arg Val 30 Leu Val Phe	
<211> 1698 <212> PRT <213> Hepatitis <400> 91 Pro Gly Ile Thr	Thr Ala Ile Glu (5) Asn Ala Val Val Val Val Val Val Val Val Val V	10 Val Arg Pro Phe Leu 25 Met Gln Pro Arg Gln 45 Pro Ile Gln Arg Val	Ser Arg Val 30 Leu Val Phe Ile His Asn	
<pre>&lt;211&gt; 1698 &lt;212&gt; PRT &lt;213&gt; Hepatitis  &lt;400&gt; 91 Pro Gly Ile Thr</pre>	Thr Ala Ile Glu C 5  Asn Ala Val Val V  Leu Ile Asn Leu M 40  Leu Trp Asn His F 55  Tyr Cys Arg Ala A	10 Val Arg Pro Phe Leu 25 Met Gln Pro Arg Gln 45 Pro Ile Gln Arg Val 60 Arg Ala Gly Arg Cys	Ser Arg Val 30  Leu Val Phe  Ile His Asn  Leu Glu Val 80	
<pre>&lt;211&gt; 1698 &lt;212&gt; PRT &lt;213&gt; Hepatitis  &lt;400&gt; 91 Pro Gly Ile Thr</pre>	Thr Ala Ile Glu Construction of the state of	10 Val Arg Pro Phe Leu 25 Met Gln Pro Arg Gln 45 Pro Ile Gln Arg Val 60 Arg Ala Gly Arg Cys 75 Asp Asn Pro Asn Val	Ser Arg Val 30 Leu Val Phe Ile His Asn Leu Glu Val 80 Leu His Arg	

		115					120					125			
Leu	Pro 130	Pro	Ala	Asp	Arg	Thr 135	Tyr	Cys	Phe	Asp	Gly 140	Phe	Ser	Arg	Cys
Ala 145	Phe	Ala	Ala	Glu	Thr 150	Gly	Val	Ala	Leu	Tyr 155	Ser	Leu	His	Asp	Leu 160
Trp	Pro	Ala	Asp	Val 165	Ala	Glu	Ala	Met	Ala 170	Arg	His	Gly	Xaa	Thr 175	Arg
Leu	Tyr	Ala	Ala 180	Leu	His	Leu	Pro	Pro 185	Glu	Val	Leu	Leu	Pro 190	Pro	Gly
Thr	Tyr	His 195	Thr	Thr	Ser	Tyr	Leu 200	Leu	Ile	His	Asp	Gly 205	Asp	Arg	Ala
Val	Val 210	Thr	Tyr	Glu	Gly	Asp 215	Thr	Ser	Ala	Gly	Tyr 220	Asn	His	Asp	Val
Ser 225	Ile	Leu	Arg	Ala	Trp 230	Ile	Arg	Thr	Thr	Lys 235	Ile	Val	Gly	Asp	His 240
Pro	Leu	Val	Ile	Glu 245	Arg	Val	Arg	Ala	Ile 250	Gly	Cys	His	Phe	Val 255	Leu
Leu	Leu	Thr	Ala 260	Ala	Pro	Glu	Pro	Ser 265	Pro	Met	Pro	Tyr	Val 270	Pro	Tyr
Pro	Arg	Ser 275	Thr	Glu	Val	Tyr	Val 280	Arg	Ser	Ile	Phe	Gly 285	Pro	Gly	Gly
Ser	Pro 290	Ser	Leu	Phe	Pro	Ser 295	Ala	Cys	Ser	Thr	Lys 300	Ser	Thr	Phe	His
Ala 305	Val	Pro	Val	His	Ile 310	Trp	Asp	Arg	Leu	Met 315	Leu	Phe	Gly	Ala	Thr 320
Leu	Asp	Asp	Gln	Ala 325	Phe	Cys	Cys	Ser	Arg 330	Leu	Met	Thr	Tyr	Leu 335	Arg
Gly	Ile	Ser	Tyr 340	Lys	Val	Thr	Val	Gly 345	Ala	Leu	Val	Ala	Asn 350	Glu	Gly
Trp	Asn	Ala 355	Ser	Glu	Asp	Ala	Leu 360	Thr	Ala	Xaa	Ile	Thr 365	Ala	Ala	Tyr
Leu	Thr 370	Ile	Cys	His	Gln	Arg 375	Tyr	Leu	Arg	Thr	Gln 380	Ala	Ile	Ser	Lys
Gly 385	Met	Arg	Arg	Leu	Gly 390	Val	Glu	His	Ala	Gln 395	Lys	Phe	Ile	Thr	Arg 400
Leu	Tyr	Ser	Trp	Leu 405	Phe	Glu	Lys	Ser	Gly 410	Arg	Asp	Tyr	Ile	Pro 415	Gly
Arg	Gln	Leu	Gln	Phe	Tyr	Ala	Gln	Cys	Arg	Arg	Trp	Leu	Ser	Ala	Gly

			420					425					430		
Phe	His	Leu 435	Asp	Pro	Arg	Val	Leu 440	Val	Phe	Asp	Glu	Ser 445	Val	Pro	Cys
Arg	Cys 450	Arg	Thr	Phe	Leu	Lys 455	Lys	Val	Ala	Gly	Lys 460	Phe	Cys	Cys	Phe
Met 465	Arg	Trp	Leu	Gly	Gln 470	Glu	Cys	Thr	Cys	Phe 475	Leu	Glu	Pro	Ala	Glu 480
Gly	Leu	Val	Gly	Asp 485	His	Gly	His	Asp	Asn 490	Glu	Ala	Tyr	Glu	Gly 495	Ser
Glu	Val	Asp	Pro 500	Ala	Glu	Pro	Ala	His 505	Leu	Asp	Val	Ser	Gly 510	Thr	Tyr
Ala	Val	His 515	Gly	His	Gln	Leu	Glu 520	Ala	Leu	Tyr	Arg	Ala 525	Leu	Asn	Val
Pro	Gln 530	Asp	Ile	Ala	Ala	Arg 535	Ala	Ser	Arg	Leu	Thr 540	Ala	Thr	Val	Glu
Leu 545	Val	Ala	Ser	Pro	Asp 550	Arg	Leu	Glu	Cys	Arg 555	Thr	Val	Leu	Gly	Asn 560
Lys	Thr	Phe	Arg	Thr 565	Thr	Val	Val	Asp	Gly 570	Ala	His	Lėu	Glu	Ala 575	Asn
Gly	Pro	Glu	Gln 580	Tyr	Val	Leu	Ser	Phe 585	Asp	Ala	Ser	Arg	Gln 590	Ser	Met
Gly	Ala	Gly 595	Ser	His	Ser	Leu	Thr 600	Tyr	Glu	Leu	Thr	Pro 605	Ala	Gly	Leu
Gln	Val 610	Arg	Ile	Ser	Ser	Asn 615	Gly	Leu	Asp	Cys	Thr 620	Ala	Thr	Phe	Pro
Pro 625	Gly	Gly	Ala	Pro	Ser 630	Ala	Ala	Pro	Gly	Glu 635	Val	Ala	Ala	Phe	Cys 640
Ser	Ala	Leu	Tyr	Arg 645	Tyr	Asn	Arg	Phe	Thr 650	Gln	Arg	His	Ser	Leu 655	Thr
Gly	Gly	Leu	Trp 660	Leu	His	Pro	Glu	Gly 665	Leu	Leu	Gly	Ile	Phe 670	Pro	Pro
Phe	Ser	Pro 675	Gly	His	Ile	Trp	Glu 680	Ser	Ala	Asn	Pro	Phe 685	Cys	Gly	Glu
Gly	Thr 690	Leu	Tyr	Thr	Arg	Thr 695	Trp	Ser	Thr	Ser	Gly 700	Phe	Ser	Ser	Asp
Phe 705	Ser	Pro	Pro	Glu	Ala 710	Ala	Ala	Pro	Ala	Met 715	Ala	Ala 、	Thr	Pro	Gly 720
Leu	Pro	His	Ser	Thr	Pro	Pro	Val	Ser	Asp	Ile	Trp	Val	Leu	Pro	Pro

725 730 735 Pro Ser Glu Glu Phe Gln Val Asp Ala Pro Val Pro Pro Ala Pro 745 Asp Pro Ala Gly Leu Pro Gly Pro Val Val Leu Thr Pro Pro Pro Pro 760 Pro Pro Val His Lys Pro Ser Ile Pro Pro Pro Ser Arg Asn Arg Arg Leu Leu Tyr Thr Tyr Pro Asp Gly Ala Lys Val Tyr Ala Gly Ser Leu Phe Glu Ser Asp Cys Asp Trp Leu Val Asn Ala Ser Asn Pro Gly His Arg Pro Gly Gly Leu Cys His Ala Phe Tyr Gln Arg Phe Pro Glu 825 Ala Phe Tyr Pro Thr Glu Phe Ile Met Arg Glu Gly Leu Ala Ala Tyr Thr Leu Thr Pro Arg Pro Ile Ile His Ala Val Ala Pro Asp Tyr Arg 855 Val Glu Gln Asn Pro Lys Arg Leu Glu Ala Ala Tyr Arg Glu Thr Cys Ser Arg Arg Gly Thr Ala Ala Tyr Pro Leu Leu Gly Ser Gly Ile Tyr 890 885 Gln Val Pro Val Ser Leu Ser Phe Asp Ala Trp Glu Arg Asn His Arg 900 905 Pro Gly Asp Glu Leu Tyr Leu Thr Glu Pro Ala Ala Asn Trp Phe Glu 920 Ala Asn Lys Pro Ala Gln Pro Val Leu Thr Ile Thr Glu Asp Thr Ala 930 935 Arg Thr Ala Asn Leu Ala Leu Glu Ile Asp Ala Ala Thr Glu Val Gly 950 955 Arg Ala Cys Ala Gly Cys Thr Ile Ser Pro Gly Ile Val His Tyr Gln Phe Thr Ala Gly Val Pro Gly Ser Gly Lys Ser Arg Ser Ile Gln Gln Gly Asp Val Asp Val Val Val Pro Thr Arg Glu Leu Arg Asn Ser Trp Arg Arg Gly Phe Ala Ala Phe Thr Pro His Thr Ala Ala Arg Val Thr Ile Gly Arg Arg Val Val Ile Asp Glu Ala Pro Ser Leu Pro

025 1030	1035	1040
Pro His Leu Leu Leu	His Met Gln Arg Ala Ser	Ser Val His Leu
1045	1050	1055
Leu Gly Asp Pro Asn Gln	Ile Pro Ala Ile Asp Phe	Glu His Ala Gly
1060	1065	1070
Leu Val Pro Ala Ile Arg	Pro Glu Leu Ala Pro Thr	Ser Trp Trp Xaa
1075	1080 1	.085
	Ala Asp Val Cys Glu Leu 1095 1100	Ile Arg Gly Ala
Tyr Pro Lys Ile Gln Thr	Thr Ser Arg Val Leu Arg	Ser Leu Phe Trp
105 1110	1115	1120
Asn Glu Pro Ala Ile Gly	Gln Lys Leu Val Xaa Thr	Gln Ala Ala Lys
1125	1130	1135
Ala Ala Asn Pro Gly Ala	Ile Thr Val His Glu Ala	Gln Gly Ala Thr
1140	1145	1150
Phe Thr Glu Thr Thr Ile	Ile Ala Thr Ala Asp Ala	Arg Gly Leu Ile
1155	1160 1	.165
_	Ala Ile Val Ala Leu Thr 1175 1180	Arg His Thr Glu
Lys Cys Val Ile Leu Asp	Ala Pro Gly Leu Leu Arg	Glu Val Gly Ile
185 . 1190	1195	1200
Ser Asp Val Ile Val Asn	Asn Phe Phe Leu Ala Gly	Gly Glu Val Gly
1205	1210	1215
Xaa His Arg Pro Ser Val	Ile Pro Arg Gly Asn Pro	Asp Gln Asn Leu
1220	1225	1230
Gly Thr Leu Gln Ala Phe	Pro Pro Ser Cys Gln Ile	Ser Ala Tyr His
1235	1240 1	245
	Gly His Arg Pro Ala Pro 1255 1260	Val Ala Ala Val
Leu Pro Pro Cys Pro Glu	Leu Glu Gln Gly Leu Leu	Tyr Met Pro Gln
265 1270	1275	1280
Glu Leu Thr Val Ser Asp	Ser Val Leu Val Phe Glu	Leu Thr Asp Ile
1285	1290	1295
Val His Cys Arg Met Ala	Ala Pro Ser Gln Arg Lys	Ala Val Leu Ser
1300	1305	1310
Thr Leu Val Gly Arg Tyr	Gly Arg Arg Thr Lys Leu	Tyr Glu Ala Ala
1315	1320 1	325
His Ser Asp Val Arg Glu	Ser Leu Ala Arg Phe Ile	Pro Thr Ile Gly

1330	1335		1340	
Pro Val Gln Al 345	a Thr Thr Cys 1350	Glu Leu Tyr	Glu Leu Val 1355	Glu Ala Met 1360
Val Glu Lys Gl	y Gln Asp Gly 1365	Ser Ala Val		Asp Leu Cys 1375
Asn Arg Asp Va	_	Thr Phe Phe 1385	=	Cys Asn Lys 1390
Phe Thr Thr Gl 1395	-	Ala His Gly 1400	v Lys Val Gly 1405	Gln Gly Ile
Ser Ala Trp Se 1410	r Lys Thr Phe 1415		Phe Gly Pro 1420	Trp Phe Arg
Ala Ile Glu Ly 425	s Glu Ile Leu 1430	Ala Leu Leu	Pro Pro Asn 1435	Ile Phe Tyr 1440
Gly Asp Ala Ty	r Glu Glu Ser 1445	Val Phe Ala 1450		Ser Gly Ala 1455
Gly Ser Cys Me		Asn Asp Phe 1465		Asp Ser Thr 1470
Gln Asn Asn Ph 1475		Leu Glu Cys 1480	Val Val Met 1485	Glu Glu Cys
Gly Met Pro Gl 1490	n Trp Leu Ile 1495		His Leu Val 1500	Arg Ser Ala
Trp Ile Leu Gl 505	n Ala Pro Lys 1510	Glu Ser Leu	Lys Gly Phe 1515	Trp Lys Lys 1520
His Ser Gly Gl	u Pro Gly Thr 1525	Leu Leu Trp 1530		Trp Asn Met 1535
Ala Ile Ile Al 154	-	Glu Phe Arg 1545		Val Ala Ala 1550
Phe Lys Gly As 1555	-	Val Leu Cys 1560	Ser Asp Tyr 1565	Arg Gln Ser
Arg Asn Ala Al 1570	a Ala Leu Ile 1575	Ala Gly Cys	Gly Leu Lys 1580	Leu Lys Val
Asp Tyr Arg Pr 585	o Ile Gly Leu 1590	Tyr Ala Gly	Val Val Val 1595	Ala Pro Gly 1600
Leu Gly Thr Le	u Pro Asp Val 1605	Val Arg Phe 1610		Leu Ser Glu 1615
Lys Asn Trp Gl	-	Glu Arg Ala 1625		Arg Leu Ala 1630
Val Cys Asp Ph	e Leu Arg Gly	Leu Thr Asn	Val Ala Gln	Val Cys Val

1635 1640 1645

Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly Leu Val His Asn 1650 1655 1660

Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys Ala His Phe Thr 665 1670 1675 1680

Glu Thr Ile Lys Pro Val Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg 1685 1690 1695

Val Glu

<210> 92

<211> 660

<212> PRT

<213> Hepatitis E virus

<400> 92

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1 5 10

Leu Pro Met Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser Gly Arg Arg 15 20 25

Arg Gly Arg Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp Ser Asp Arg 30 35 40 45

Val Asp Ser Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro 50 55 60

Phe Ala Ala Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg 65 70 75

Gln Pro Pro Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln Ser Lys Arg 80 85 90

Pro Ser Val Ala Pro Arg Arg Ser Thr Pro Ala Gly Ala Ala Pro 95 100 105

Leu Thr Ala Ile Ser Pro Ala Pro Asp Thr Ala Pro Val Pro Asp Val 10 115 120 125

Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser 130 135 140

Pro Leu Thr Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala 145 150 155

Ala Pro Leu Asn Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His 160 165 170

Ile Met Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Val Arg 175 180 185

Ala Thr Ile Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr

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US5P243A/20

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			_		gag Glu	_		_		_		_		_	_	293
_		_		_	cac His	_					_				-	341
_					ctt Leu	_										389
		_			cgt Arg				_		_	-	_			437
_	_				cct Pro 140	_	_	_			_		_			485
	_	_	_		gct Ala	_					_				_	533
	_				gct Ala	_	_	-		-	_	_	_			581
					gcc Ala											629
					cac His			_						-		677
	_	_	_	_	act Thr 220				_		_					725
					ctt Leu											773
					gtc Val											821

.

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									_				ttt Phe	917
					_				_	_			aaa Lys	965
		_	_	_	_				_	_		_	ctc Leu 325	1013
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			_	_	aag Lys 620						_	_			_	1925
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Ser	Ser	Asp	Phe	Ser 715	Pro	Pro	Glu	Ala	Ala 720	Ala	Pro	Ala	Ser	Ala 725	Ala	
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	_		_		gct Ala		_		_			_				2357
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				_	ccc Pro					_		_				2549
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	-	-			tta Leu 860		_	_			Ile		_		_	2645
	_			_	gag Glu			_	_				_			2693
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	act atc ggc cgc cgc Thr Ile Gly Arg Arg 1040		
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	gtc ccc gcg atc cgc Val Pro Ala Ile Arg 1085		_
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			cta gcg agg ttt atc Leu Ala Arg Phe Ile 1350	: `
Pro Thr Ile Gly I			gag ctg tac gag ctg Glu Leu Tyr Glu Leu 1365	
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				g gcc cta ctc 1 Ala Leu Leu		4373
Asn Ile Phe		Ala Tyr		n gtg ttt gct Val Phe Ala 1460	Ala Ala	4421
				a aat gac ttc 1 Asn Asp Phe 1475		4469
	Thr Gln Asn			ctt gag tgt Leu Glu Cys 1490		4517
				agg ttg tac Arg Leu Tyr	_	4565
Val Arg Ser	Ala Trp Ile 1515	Leu Gln	Ala Pro Lys 1520		Lys Gly 1525	4613
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Ala Arg Ala Gly Arg Cys Leu Glu Val Gly Ala His Pro Arg Ser Ile 85 90 95	
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Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro Thr Arg Gly Pro Ala Ala 115 120 125	
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Tyr Cys Phe Asp Gly Phe Ser Arg Cys Ala Phe Ala Ala Glu Thr Gly	

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Ala	Met	Ala	Arg 180	His	Gly	Met	Thr	Arg 185	Leu	Tyr	Ala	Ala	Leu 190	His	Leu
Pro	Pro	Glu 195	Val	Leu	Leu	Pro	Pro 200	Gly	Thr	Tyr	His	Thr 205	Thr	Ser	Tyr
Leu	Leu 210	Ile	His	Asp	Gly	Asn 215	Arg	Ala	Val	Val	Thr 220	Tyr	Glu	Gly	Asp
Thr 225	Ser	Ala	Gly	Tyr	Asn 230	His	Asp	Val	Ser	Ile 235		Arg	Ala	Trp	Ile 240
Arg	Thr	Thr	Lys	Ile 245	Val	Gly	Asp	His	Pro 250	Leu	Val	Ile	Glu	Arg 255	Val
Arg	Ala	Ile	Gly 260	Cys	His	Phe	Val	Leu 265	Leu	Leu	Thr	Ala	Ala 270	Pro	Glu
Pro	Ser	Pro 275	Met	Pro	Tyr	Val	Pro 280	Tyr	Pro	Arg	Ser	Thr 285	Glu	Val	Tyr
Val	Arg 290	Ser	Ile	Phe	Gly	Pro 295	Gly	Gly	Ser	Pro	Ser 300	Leu	Phe	Pro	Ser
Ala 305	Cys	Ser	Thr	Lys	Ser 310	Thr	Phe	His	Ala	Val 315	Pro	Val	His	Ile	Trp 320
Asp	Xaa	Leu	Met	Leu 325	Phe	Gly	Ala	Thr	Leu 330	Xaa	Asp	Gln	Ala	Phe 335	Cys
Cys	Ser	Arg	Leu 340	Met	Thr	Tyr	Leu	Arg 345	Gly	Ile	Ser	Tyr	Lys 350	Val	Thr
Val	Gly	Ala 355		Val	Ala	Asn	Glu 360	Gly	Trp	Asn	Ala	Ser 365	Glu	Asp	Ala
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Gln	Cys	Arg 435	Arg	Trp	Leu	Ser	Ala 440	Gly	Phe	His	Leu	Xaa 445	Pro	Arg	Xaa
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Cys	Thr	Cys	Phe	Leu 485	Glu	Pro	Ala	Glu	Gly 490	Leu	Val	Gly	Asp	Gln 495	Gly
His	Asp	Asn	Glu 500	Ala	Tyr	Glu	Gly	Ser 505	Glu	Val	Asp	Pro	Ala 510	Glu	Pro
Ala	His	Leu 515	Asp	Val	Ser	Gly	Thr 520	Tyr	Ala	Val	His	Gly 525	His	Gln	Leu
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Ala 545	Ser	Arg	Leu	Thr	Ala 550	Thr	Val	Glu	Leu	Val 555	Ala	Ser	Pro	Asp	Arg 560
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Val	Asp	Gly	Ala 580	His	Leu	Glu	Ala	Asn 585	Gly	Pro	Glu	Glu	Tyr 590	Val	Leu
Ser	Phe	Asp 595	Ala	Ser	Arg	Gln	Ser 600	Met	Gly	Ala	Gly	Ser 605	His	Ser	Leu
Thr	Tyr 610	Glu	Leu	Thr	Pro	Ala 615	Gly	Leu	Gln	Val	Lys 620	Ile	Ser	Ser	Asn
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755 765 760 Pro Ile Val Leu Thr Pro Pro Pro Pro Pro Pro Pro Val Arg Lys Pro 775 Ala Thr Ser Pro Pro Pro Arg Thr Arg Arg Leu Leu Tyr Thr Tyr Pro 795 Asp Gly Ala Lys Val Tyr Ala Gly Ser Leu Xaa Glu Ser Asp Cys Asp 810 Trp Leu Val Asn Ala Ser Asn Pro Gly His Arg Pro Gly Gly Leu 825 Cys His Ala Phe Tyr Gln Arg Phe Pro Glu Ala Phe Tyr Ser Thr Glu Phe Ile Met Arg Glu Gly Leu Ala Ala Tyr Thr Leu Thr Pro Arg Pro Ile Ile His Ala Val Ala Pro Asp Tyr Arg Val Glu Gln Asn Pro Lys 870 Arg Leu Glu Ala Ala Tyr Arg Glu Thr Cys Ser Arg Arg Gly Thr Ala 890 Ala Tyr Pro Leu Leu Gly Ser Gly Ile Tyr Gln Val Pro Val Ser Leu Ser Phe Asp Ala Trp Glu Arg Asn His Arg Pro Gly Asp Glu Leu Tyr 920 Leu Thr Glu Pro Ala Ala Ala Trp Phe Glu Ala Asn Lys Pro Ala Gln 930 935 Pro Ala Leu Thr Ile Thr Glu Asp Thr Ala Arg Thr Ala Asn Leu Ala 955 Leu Glu Ile Asp Ala Ala Thr Glu Val Gly Arg Ala Cys Ala Gly Cys Thr Ile Ser Pro Gly Ile Val His Tyr Gln Phe Thr Ala Gly Val Pro 985 Gly Ser Gly Lys Ser Arg Ser Ile Gln Gly Asp Val Asp Val Val Val Val Pro Thr Arg Glu Leu Arg Asn Ser Trp Arg Arg Arg Gly Phe Ala Ala Phe Thr Pro His Thr Ala Ala Arg Val Thr Ile Gly Arg Arg Val Val Ile Asp Glu Ala Pro Ser Leu Pro Pro His Leu Leu Leu 1050 His Met Gln Arg Ala Ser Ser Val His Leu Leu Gly Asp Pro Asn Gln

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Cys Glu Leu Tyr Glu Leu Val Glu Ala Met Val Glu Lys Gly Gln Asp

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Ile Thr Phe Phe Gln Ly	ys Asp Cys Asn Lys 1400	Phe Thr Thr Gly Glu Thr 1405
Ile Ala His Gly Lys Va	al Gly Gln Gly Ile	Ser Ala Trp Ser Lys Thr
1410	1415	1420
Phe Cys Ala Leu Phe G 425		Ala Ile Glu Lys Glu Ile 1435 1440
Leu Ala Leu Leu Pro Pr	ro Asn Ile Phe Tyr	Gly Asp Ala Tyr Glu Glu
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Ser Val Phe Ala Ala A	la Val Ser Gly Ala	Gly Ser Cys Met Val Phe
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Glu Asn Asp Phe Ser G	lu Phe Asp Ser Thr 1480	Gln Asn Asn Phe Ser Leu 1485
Gly Leu Glu Cys Val Va	al Met Glu Glu Cys	Gly Met Pro Gln Trp Leu
1490	1495	1500
Ile Arg Leu Tyr His Le 505 15:		Trp Ile Leu Gln Ala Pro .515 1520
Lys Glu Ser Leu Lys G	ly Phe Trp Lys Lys	His Ser Gly Glu Pro Gly
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Val Val Leu Cys Ser As	sp Tyr Arg Gln Xaa	Arg Asn Ala Ala Ala Leu
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Pro Glu Arg Ala Glu Gl	ln Leu Arg Leu Ala	Val Cys Asp Phe Leu Arg
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1650	1655	1660
Tyr Gly Val Ser Pro Gl	ly Leu Val His Asn	Leu Ile Gly Met Leu Gln

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<211> 660

<212> PRT

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35 40 45

Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala 50 55 60

Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro 65 70 75 80

Arg Pro Leu Xaa Ser Ala Trp Arg Asp Gln Ser Gln Arg Pro Ser Ala 85 90 95

Ala Pro Arg Arg Ser Ala Pro Ala Gly Ala Ala Pro Leu Thr Ala 100 105 110

Val Ser Pro Ala Pro Asp Thr Ala Pro Val Pro Asp Val Asp Ser Arg 115 120 125

Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr 130 135 140

Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu 145 150 155 160

Asn Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala 165 170 175

Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala Thr Ile 180 185 190

Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser

Ile Ser Phe Trp Pro Gln Thr Thr Thr Pro Thr Ser Val Asp Met 210 215 220

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Ala	Ser	Glu	Leu	Val 245	Ile	Pro	Ser	Glu	Arg 250	Leu	His	Tyr	Arg	Asn 255	Gln
Gly	Trp	Arg	Ser 260	Val	Glu	Thr	Thr	Gly 265	Val	Ala	Glu	Glu	Glu 270	Ala	Thr
Ser	Gly	Leu 275	Val	Met	Leu	Cys	Ile 280	His	Gly	Ser	Pro	Val 285	Asn	Ser	Tyr
Thr	Asn 290	Thr	Pro	Tyr	Thr	Gly 295	Ala	Leu	Gly	Leu	Leu 300	Asp	Phe	Ala	Leu
Glu 305	Leu	Glu	Phe	Arg	Asn 310	Leu	Thr	Pro	Gly	Asn 315	Thr	Asn	Thr	Arg	Val 320
Ser	Arg	Tyr	Thr	Ser 325	Thr	Ala	Arg	His	Arg 330	Leu	Arg	Arg	Gly	Ala 335	Asp
Gly	Thr	Ala	Glu 340	Leu	Thr	Thr	Thr	Ala 345	Ala	Thr	Arg	Phe	Met 350	Lys	Asp
Leu	His	Phe 355	Ala	Gly	Thr	Asn	Gly 360	Val	Gly	Glu	Val	Gly 365	Arg	Gly	Ile
Ala	Leu 370	Thr	Leu	Phe	Asn	Leu 375	Ala	Asp	Thr	Leu	Leu 380	Gly	Gly	Leu	Pro
Thr 385	Glu	Leu	Ile	Ser	Ser 390	Ala	Gly	Gly	Gln	Leu 395	Phe	Tyr	Ser	Arg	Pro 400
Val	Val	Ser	Ala	Asn 405	Gly	Glu	Pro	Thr	Val 410	Lys	Leu	Tyr	Thr	Ser 415	Val
Glu	Asn	Ala	Gln 420	Gln	Asp	Lys	Gly	Ile 425	Thr	Ile	Pro	His	Asp 430	Ile	Asp
Leu	Gly	Asp 435	Ser	Arg	Val	Val	Ile 440	Gln	Asp	Tyr	Asp	Asn 445	Gln	Xaa	Glu
Gln	Asp 450	Arg	Pro	Thr	Pro	Ser 455	Pro	Ala	Pro	Ser	Arg 460	Pro	Phe	Ser	Val
Leu 465	Arg	Ala	Asn	Asp	Val 470	Leu	Trp	Leu	Ser	Leu 475	Thr	Ala	Ala	Glu	Tyr 480
Asp	Gln	Thr	Thr	Tyr 485	Gly	Ser	Ser	Thr	Asn 490	Pro	Met	Tyr	Val	Ser 495	Asp
Thr	Val	Thr	Leu 500	Val	Asn	Val	Ala	Thr 505	Gly	Ala	Gln	Ala	Val 510	Ala	Arg
Ser	Leu	Asp 515	Trp	Ser	Lys	Val	Thr 520	Leu	Asp	Gly	Arg	Pro 525	Leu	Thr	Thr

Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys 535 Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro 585 Thr Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp 615 Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys 650 Thr Arg Glu Ser 660 <210> 168 <211> 122 <212> PRT <213> Hepatitis E virus <220> <223> us2 orf3 <400> 168 Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met Ser Phe His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Leu 90

Xaa Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro Pro Val

105

110

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<210> 169

<211> 33

<212> PRT

<213> Hepatitis E virus

<220>

<223> M 4-2

<400> 169

Ala Asn Gln Pro Gly His Leu Ala Pro Leu Gly Glu Ile Arg Pro Ser
1 10 15

Ala Pro Pro Leu Pro Pro Val Ala Asp Leu Pro Gln Pro Gly Leu Arg
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Arg

<210> 170

<211> 48

<212> PRT

<213> Hepatitis E virus

<220>

<223> M 3-2e

<400> 170

Thr Phe Asp Tyr Pro Gly Arg Ala His Thr Phe Asp Asp Phe Cys Pro 1 5 10 15

Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val 20 25 30

Ala Glu Leu Gln Arg Leu Lys Val Lys Val Gly Lys Thr Arg Glu Leu 35 40 45

<210> 171

<211> 33

<212> PRT

<213> Hepatitis E virus

<220>

<223> B 4-2

<400> 171

Ala Asn Pro Pro Asp His Ser Ala Pro Leu Gly Val Thr Arg Pro Ser 1 5 10 15

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Ala Pro Pro Leu Pro His Val Val Asp Leu Pro Gln Leu Gly Pro Arg
20 25 30
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Arg

<210> 172

<211> 48

<212> PRT

<213> Hepatitis E virus

<220>

<223> B 3-2e

<400> 172

Thr Leu Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro 1 5 10 15

Glu Cys Arg Pro Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val 20 25 30

Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Leu 35 40 45

<210> 173

<211> 33

<212> PRT

<213> Hepatitis E virus

<220>

<223> ORF3 (u4.2)

<400> 173

Asp Ser Arg Pro Ala Pro Ser Val Pro Leu Gly Val Thr Ser Pro Ser 1 5 10 15

Ala Pro Pro Leu Pro Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg
20 25 30

Arg

<210> 174

<211> 48

<212> PRT

<213> Hepatitis E virus

<220>

<223> ORF2 (u3.2e)

<400> 174

Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro 1 5 10 15

Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile 20 25 30

Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Ser

<210> 175

<211> 33

<212> PRT

<213> Hepatitis E virus

<220>

<223> US 4-2

<400> 175

Asp Ser Arg Pro Ala Pro Ser Val Pro Leu Gly Val Thr Ser Pro Ser 1 5 10 15

Ala Pro Pro Leu Pro Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg
20 25 30

Cys

<210> 176

<211> 48

<212> PRT

<213> Hepatitis E virus

<220>

<223> US 3-2e

<400> 176

Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro 1 5 10 15

Glu Cys Arg Thr Leu Gly Val Gln Gly Cys Ala Phe Gln Ser Thr Ile 20 25 30

Ala Glu Val Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Val 35 40 45

<210> 177

<211> 21

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<213> Hepatitis E virus
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<223> HEVConsORF1-s2
<400> 177
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ctgccytkgc gaatgctgtg g
<210> 178
<211> 24
<212> DNA
<213> Hepatitis E virus
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<223> HEVConsORF1-a2
<400> 178
ggcagwrtac carcgctgaa catc
                                                                   24
<210> 179
<211> 294
<212> DNA
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<220>
<223> z12-orf1 (G.S.)
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tgctgtggtg gttcggccgt ttttatctcg tttacagact gagattctta ttaatttgat 120
gcaaccccga cagttggtct ttcgacctga ggtgttctgg aaccatccca tccaacgtgt 180
tatacataat gaattggagc agtactgccg ggcccgggcc ggtcgctgtc tggaaattgg 240
ageceateca aggteaatea atgataatee taatgttetg categgtgtt teet
<210> 180
<211> 418
<212> DNA
<213> Hepatitis E virus
<220>
<223> z12-orf1.con
<400> 180
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atgctgtggt ggttcggccg tttttatctc gtttacagac tgagattctt attaatttga 120
tgcaaccccg acagttggtc tttcgacctg aggtgttctg gaaccatccc atccaacgtg 180
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cggtcgggag	ggacgttcag	cgctggtact	ccgccccac	ccgtggcccc	gcggccaact	360
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gatagctatt	ccacatgaca	tagatttggg	cgactctcgt	ttggtaatcc	aggattatga	180
taaccaacac	gaacaag					197
	itis E viru	ıs				
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<210> 183 <211> 25 <212> DNA <213> Hepat	itis E viru	ıs				
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<400> 183 aggggttggt	tggatgaata	taggg				25
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<223> z12-orf23.con

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agycgactgg ccgccgtcgt gggcggcgca gcggcggtgc cggcggtggt ttctggggtg 180
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<210> 185 <211> 890 <212> DNA <213> Hepatitis E virus <220>

<223> z12-3p.race

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<sup>&</sup>lt;210> 186

<sup>&</sup>lt;211> 919

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Hepatitis E virus

<220> <223> z12-3p.con

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<210> 187

<211> 138

<212> PRT

<213> Hepatitis E virus

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<223> z12-orf1.pep

<400> 187

Gly Ile Thr Thr Ala Ile Glu Gln Ala Ala Leu Gly Ala Ala Asn Ser 1 5 10 15

Ala Leu Ala Asn Ala Val Val Val Pro Phe Leu Ser Arg Leu Gln
20 25 30

Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg 35 40 45

Pro Glu Val Phe Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu 50 55 60

Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Ile Gly
65 70 75 80

Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys
85 90 95

Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro 100 105 110

Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
115 120 125

Pro Pro Val Asp Arg Thr Tyr Cys Leu Asp 130 135

<210> 188

<211> 61

<212> PRT

<213> Hepatitis E virus

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<223> z12-orf2-5'.pep

<400> 188

Met Arg Pro Arg Val Val Leu Leu Phe Leu Val Phe Leu Pro Met
1 5 10 15

Leu Pro Ala Pro Pro Ala Gly Gln Xaa Thr Gly Arg Arg Arg Gly Arg
20 25 30

Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp Gly Asp Arg Val Asp Ser 35 40 45

Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro
50 55 60

<210> 189

<211> 276

<212> PRT

<213> Hepatitis E virus

<220>

<223> z12-orf2-3'.pep

<400> 189

Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro 1 5 10 15

Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val

Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp 35 40 45

Leu Gly Asp Ser Arg Leu Val Ile Gln Asp Tyr Asp Asn Gln His Glu 55 Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val 70 Leu Arg Ala Asn Asp Ala Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr Val Thr Phe Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg 115 Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr 135 Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn 170 Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly 185 His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro 200 Val Ser Val Ser Ala Val Gly Val Leu Ala Pro His Ser Ser Leu Ala 215 Ile Leu Glu Asp Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp 235 Asp Phe Cys Pro Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys 265 Thr Arg Glu Phe 275

<210> 190

<211> 74

<212> PRT

<213> Hepatitis E virus

<220>

<223> z12-orf3.pep

<400> 190

Met Asn Asn Met Phe Cys Ala Ser Pro Met Gly Ser Pro Cys Ala Leu 1 5 10 15

Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg 20 25 30

His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala Ala Ala 35 40 45

Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser 50 55 60

Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro 65 70

<210> 191

<211> 408

<212> DNA

<213> Hepatitis E virus

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<223> pJ0orf3-29.seq

<400> 191

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ctggeegeeg tegtgggegg egeageggeg gtgeeggegg tggtttetgg ggtgacaggg 180
ttgattetea gecettegee etcecetata tteatecaae caacecette geegeegatg 240
tegttteaca accegggget ggaactegee etcgacagee geeeegeeee ettggeteeg 300
cttggegtga ceagteeeag egeeeeteeg etgeeeeeg tegtegatet geeecagett 360
ggtetgegee gegactacaa ggaegaegat gacaagtaat aaggatee 408

<210> 192

<211> 1026

<212> DNA

<213> Hepatitis E virus

<220>

<223> cksorf2m-2.seq

<400> 192

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atagacetgg gtgacteccg tgtggttate caggattatg ataaccagca tgagcaagac 360 cgacetacte cgtcacetge ecectetege ecetteteag ttettegtge caatgatgtt 420 ttgtgggettt eceteactge egetgagtat gaccagacta egtatgggte gtccaceaac 480 ecetatgtatg tetetgacac agttacgett gttaatgtgg etactggtge teaggetgtt 540 geccegetece ttgattggte taaagttact etggacggee geceettae taccatteag 600 eagtatteta agacattta tgtteteeeg eteeggga agetgteett ttgggagget 660 ggcacgacta aggeeggeta ecettacaat tataatacta eegetagtga ecaaattttg 720 attgagaatg eggeeggea eegtgteget atttecacet ataccactag ettaggtgee 780 ggtcctacet egatetete ggteggegta etggetecac actetgeeet tgeeggtet 840 gaggatacta ttgattacee egecegtgee eatactttg atgattttg eeeggagteg 900 egtaceetag gtttgeaggg ttgtgeatte eagtetacta ttgetgaget ecaagtata 1020 ggatee

<210> 193 <211> 1389 <212> DNA <213> Hepatitis E virus <220>

<223> CKSORF32M-3.seq

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<210> 194
<211> 408
<212> DNA
<213> Hepatitis E virus
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<223> plorf3-12.con

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ctggccgccg tcgtgggcgg cgcagcggcg gtgccggcgg tggtttctgg ggtgacaggg 180

ttgattctca gcccttcgcc ctcccctata ttcatccaac caaccccttc gccgccgatg 240

tcgtttcaca acccggggct ggaactcgcc ctcgacagcc gccccgccc cttggctccg 300
cttggcgtga ccagtcccag cgcccctccg ctgccccccg tcgtcgatct gccccagctt 360
ggtctgcgcc gcgactacaa ggacgacgat gacaagtaat aaggatcc

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<210> 195
<211> 1026
<212> DNA
<213> Hepatitis E virus
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<220>

#### 106/140

<223> plorf2.2-6.seq <400> 195 gaattcatgg gtgctgatgg gactgctgag cttactacca cagcagccac acgtttcatg 60 aaggacetge acttegetgg caegaatgge gttggtgagg tgggtegtgg tategeeetg 120 acactgttca atctcgctga tacgcttctc ggcggtttac cgacagaatt gatttcgtcg 180 gctgggggcc aactgtttta ctcccgcccg gttgtctcag ccaatggcga gccaacagta 240 aagttatata catctgttga gaatgcgcag caagacaagg gcatcaccat tccacatgat 300 atagacctgg gtgactcccg tgtggttatc caggattatg ataaccagca tgagcaagac 360 cgacctactc cgtcacctgc ccctctcgc cccttctcag ttcttcgtgc caatgatgtt 420 ttgtggcttt ccctcactgc cgctgagtat gaccagacta cgtatgggtc gtccaccaac 480 cctatgtatg tctctgacac agttacgctt gttaatgtgg ctactggtgc tcaggctgtt 540 geoegeteee tigatiggte taaagitaet eiggaeggee geoecettae taecaticag 600 cagtatteta agacatttta tgtteteeeg eteegeggga agetgteett ttgggagget 660 ggcacgacta aggccggcta cccttacaat tataatacta ccgctagtga ccaaattttg 720 attgagaatg eggeeggeea eegtgteget atttecacet ataccactag ettaggtgee 780 ggtcctacct cgatctctgc ggtcggcgta ctggctccac actctgccct tgccgttctt 840 gaggatacta ttgattaccc cgcccgtgcc catacttttg atgatttttg cccggagtgc 900 cgtaccctag gtttgcaggg ttgtgcattc cagtctacta ttgctgagct ccagcgttta 960 aaaatgaagg taggtaaaac ccgggagtct gactacaagg acgacgatga caagtaataa 1020 ggatcc 1026 <210> 196 <211> 1389 <212> DNA <213> Hepatitis E virus <223> PLORF32M-14-5.seq <400> 196 gaattcatga ataacatgtc ttttgcatcg cccatgggat caccatgcgc cctagggctg 60 ttctgttgtt gctcttcgtg cttttgccta tgctgcccgc gccaccggcc agccagccgt 120

ctggccgccg tcgtgggcgg cgtagcggcg gtgccggcgg tggtttctgg ggtgacaggg 180

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<210> 197

#### 107/140

tegttteaca accegggget ggaactegee etegacagee geecegeece ettggeteeg 300 ettggegtga eeagteeeag egeceeteeg etgeeeeeg tegtegatet geeeeagett 360 ggtctgcgcc gcggtgctga tgggactgct gagcttacta ccacagcagc cacacgtttc 420 atgaaggacc tgcacttcgc tggcacgaat ggcgttggtg aggtgggtcg tggtatcgcc 480 ctgacactgt tcaatctcgc tgatacgctt ctcggcggtt taccgacaga attgatttcg 540 teggetgggg gecaactgtt ttacteeege eeggttgtet eagecaatgg egagecaaca 600 gtaaagttat atacatctgt tgagaatgcg cagcaagaca agggcatcac cattccacat 660 gatatagacc tgggtgactc ccgtgtggtt atccaggatt atgataacca gcatgagcaa 720 gaccgaccta ctccgtcacc tgccccctct cgccccttct cagttcttcg tgccaatgat 780 gttttgtggc tttccctcac tgccgctgag tatgaccaga ctacgtatgg gtcgtccacc 840 aaccctatgt atgtctctga cacagttacg cttgttaatg tggctactgg tgctcaggct 900 gttgcccgct cccttgattg gtctaaagtt actctggacg gccgcccct tactaccatt 960 cagcagtatt ctaagacatt ttatgttctc ccgctccgcg ggaagctgtc cttttgggag 1020 gctggcacga ctaaggccgg ctacccttac aattataata ctaccgctag tgaccaaatt 1080 ttgattgaga atgcggccgg ccaccgtgtc gctatttcca cctataccac tagcttaggt 1140 geoggteeta cetegatete tgeggtegge gtaetggete cacactetge cettgeegtt 1200 cttgaggata ctattgatta ccccgcccgt gcccatactt ttgatgattt ttgcccggag 1260 tgccgtaccc taggtttgca gggttgtgca ttccagtcta ctattgctga gctccagcgt 1320 ttaaaaatga aggtaggtaa aacccgggag tctgactaca aggacgacga tgacaagtaa 1380 taaggatcc 1389

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<211> 74
<212> PRT
<213> Hepatitis E virus

<220>
<223> z12-orf3-5'.pep

<400> 197
Met Asn Asn Met Phe Cys Ala Ser Pro Met Gly Ser Pro Cys Ala Leu
1 5 10 15
Cly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Pro Arg
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Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg
20 25 30

His Arg Pro Ala Xaa Arg Leu Ala Ala Val Val Gly Gly Ala Ala Ala 35 40 45

Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser 50 55 60

Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro 65 70

<210> 198

<211> 63

<212> DNA

<213> Hepatitis E virus

<220>

<223> Description of Artificial Sequence: Primer orf23p

<400> 198

tatatggatc cttattactt gtcatcgtcg tccttgtagt cagactcccg ggttttacct 60

acc 63

<210> 199

<211> 338

<212> PRT

<213> Hepatitis E virus

<220>

<223> cksorf2m-2.pep

<400> 199

Glu Phe Met Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala 1 5 10 15

Thr Arg Phe Met Lys Asp Leu His Phe Ala Gly Thr Asn Gly Val Gly 20 25 30

Glu Val Gly Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr 35 40 45

Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln
50 60

Leu Phe Tyr Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val 65 70 75 80

Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr 85 90 95

Ile Pro His Asp Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp
100 105 110

Tyr Asp Asn Gln His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro 115 120 125

Ser Arg Pro Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser 135 Leu Thr Ala Ala Glu Tyr Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn 155 Pro Met Tyr Val Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly 165 170 Ala Gln Ala Val Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys 215 Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr 250 Ser Leu Gly Ala Gly Pro Thr Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala 280 Arg Ala His Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly 290 295 Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu 310 315 Lys Met Lys Val Gly Lys Thr Arg Glu Ser Asp Tyr Lys Asp Asp Asp

Asp Lys

<210> 200

<211> 338

<212> PRT

<213> Hepatitis E virus

<220>

<223> plorf2.2-6.pep

<400> 200

Glu Phe Met Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala 1 5 10 15

Thr Arg Phe Met Lys Asp Leu His Phe Ala Gly Thr Asn Gly Val Gly
20 25 30

Glu	Val	Gly 35	Arg	Gly	Ile	Ala	Leu 40	Thr	Leu	Phe	Asn	Leu 45	Ala	Asp	Thr
Leu	Leu 50	Gly	Gly	Leu	Pro	Thr 55	Glu	Leu	Ile	Ser	Ser 60	Ala	Gly	Gly	Gln
Leu 65	Phe	Tyr	Ser	Arg	Pro 70	Val	Val	Ser	Ala	Asn 75	Gly	Glu	Pro	Thr	Val 80
Lys	Leu	Tyr	Thr	Ser 85	Val	Glu	Asn	Ala	Gln 90	Gln	Asp	Lys	Gly	Ile 95	Thr
Ile	Pro	His	Asp 100	Ile	Asp	Leu	Gly	Asp 105	Ser	Arg	Val	Val	Ile 110	Gln	Asp
Tyr	Asp	Asn 115	Gln	His	Glu	Gln	Asp 120	Arg	Pro	Thr	Pro	Ser 125	Pro	Ala	Pro
Ser	Arg 130	Pro	Phe	Ser	Val	Leu 135	Arg	Ala	Asn	Asp	Val 140	Leu	Trp	Leu	Ser
Leu 145	Thr	Ala	Ala	Glu	Tyr 150	Asp	Gln	Thr	Thr	Tyr 155	Gly	Ser	Ser	Thr	Asn 160
Pro	Met	Tyr	Val	Ser 165	Asp	Thr	Val	Thr	Leu 170	Val	Asn	Val	Ala	Thr 175	Gly
Ala	Gln	Ala	Val 180	Ala	Arg	Ser	Leu	Asp 185	Trp	Ser	Lys	Val	Thr 190	Leu	Asp
Gly	Arg	Pro 195	Leu	Thr	Thr	Ile	Gln 200	Gln	Tyr	Ser	Lys	Thr 205	Phe	Tyr	Val
Leu	Pro 210	Leu	Arg	Gly	Lys	Leu 215	Ser	Phe	Trp	Glu	Ala 220	Gly	Thr	Thr	Lys
Ala 225	Gly	Tyr	Pro	Tyr	Asn 230	Tyr	Asn	Thr	Thr	Ala 235	Ser	Asp	Gln	Ile	Leu 240
Ile	Glu	Asn	Ala	Ala 245	Gly	His	Arg	Val	Ala 250	Ile	Ser	Thr	Tyr	Thr 255	Thr
Ser	Leu	Gly	Ala 260	Gly	Pro	Thr	Ser	Ile 265	Ser	Ala	Val	Gly	Val 270	Leu	Ala
Pro	His	Ser 275	Ala	Leu	Ala	Val	Leu 280	Glu	Asp	Thr	Ile	Asp 285	Tyr	Pro	Ala
Arg	Ala 290	His	Thr	Phe	Asp	Asp 295	Phe	Cys	Pro	Glu	Cys 300	Arg	Thr	Leu	Gly
Leu 305	Gln	Gly	Cys	Ala	Phe 310	Gln	Ser	Thr	Ile	Ala 315	Glu	Leu	Gln	Arg	Leu 320
Lys	Met	Lys	Val	Gly 325	Lys	Thr	Arg	Glu	Ser 330	Asp	Tyr	Lys	Asp	Asp 335	Asp

Asp Lys

<210> 201 <211> 37 <212> DNA <213> Hepatitis E virus	
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<400> 202 tatatggatc cttattactt gtcatcgtcg tccttgtagt cgcggcgcag accaagctgg @	50
ggcagatc	68
<210> 203 <211> 132 <212> PRT <213> Hepatitis E virus	
<220> <223> pJOorf3-29.pep	
<400> 203 Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys 1 5 10 15	
Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys 20 25 30	
Pro Arg His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala 35 40 45	
Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser 50 55 60	
Pro Ser Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met 65 70 75 80	
Ser Phe His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala 85 90 95	

Pro Leu Ala Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro 100 105 110

Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Asp Tyr Lys Asp 115 120 125

Asp Asp Asp Lys 130

<210> 204

<211> 132

<212> PRT

<213> Hepatitis E virus

<220>

<223> plorf3-12.pep

<400> 204

Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys

1 10 15

Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys 20 25 30

Pro Arg His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala
35 40 45

Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser 50 55 60

Pro Ser Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met 65 70 75 80

Ser Phe His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala 85 90 95

Pro Leu Ala Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro 100 105 110

Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Asp Tyr Lys Asp 115 120 125

Asp Asp Asp Lys 130

<210> 205

<211> 48

<212> DNA

<213> Hepatitis E virus

<220>

<223> Description of Artificial Sequence: Primer orf23

<400> 205

#### ctcagcagtc ccatcagcac cgcggcgcag accaagctgg ggcagatc

<210> 206 <211> 459 <212> PRT <213> Hepatitis E virus <220> <223> CKSORF32M-3.pep <400> 206 Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys 2.5 Pro Arg His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Val Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met Ser Phe His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala 90 Pro Leu Ala Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro 100 Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Gly Ala Asp Gly 120 Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu 130 His Phe Ala Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala 150 155 Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp Leu

Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln

235

230

		_	_	_	_	_		_	_					<b>-</b>	_
Asp	Arg	Pro	Thr	Pro 245	Ser	Pro	Ala	Pro	Ser 250	Arg	Pro	Phe	Ser	Val 255	Leu
Arg	Ala	Asn	Asp 260	Val	Leu	Trp	Leu	Ser 265	Leu	Thr	Ala	Ala	Glu 270	Tyr	Asp
Gln	Thr	Thr 275	Tyr	Gly	Ser	Ser	Thr 280	Asn	Pro	Met	Tyr	Val 285	Ser	Asp	Thr
Val	Thr 290	Leu	Val	Asn	Val	Ala 295	Thr	Gly	Ala	Gln	Ala 300	Val	Ala	Arg	Ser
Leu 305	Asp	Trp	Ser	Lys	Val 310	Thr	Leu	Asp	Gly	Arg 315	Pro	Leu	Thr	Thr	Ile 320
Gln	Gln	Tyr	Ser	Lys 325	Thr	Phe	Tyr	Val	Leu 330	Pro	Leu	Arg	Gly	Lys 335	Leu
Ser	Phe	Trp	Glu 340	Ala	Gly	Thr	Thr	Lys 345	Ala	Gly	Tyr	Pro	Tyr 350	Asn	Tyr
Asn	Thr	Thr 355	Ala	Ser	Asp	Gln	Ile 360	Leu	Ile	Glu	Asn	Ala 365	Ala	Gly	His
Arg	Val 370	Ala	Ile	Ser	Thr	Tyr 375	Thr	Thr	Ser	Leu	Gly 380	Ala	Gly	Pro	Thr
Ser 385	Ile	Ser	Ala	Val	Gly 390	Val	Leu	Ala	Pro	His 395	Ser	Ala	Leu	Ala	Val 400
Leu	Glu	Asp	Thr	Ile 405	Asp	Tyr	Pro	Ala	Arg 410	Ala	His	Thr	Phe	Asp 415	Asp
Phe	Cys	Pro	Glu 420	Cys	Arg	Thr	Leu	Gly 425	Leu	Gln	Gly	Cys	Ala 430	Phe	Gln
Ser	Thr	Ile 435	Ala	Glu	Leu	Gln	Arg 440	Leu	Lys	Met	Lys	Val 445	Gly	Lys	Thr
Arg	Glu 450	Ser	Asp	Tyr	Lys	Asp 455	Asp	Asp	Asp	Lys					
<211	)> 20 L> 45	59													

<210> 207 <211> 459 <212> PRT <213> Hepatitis E virus

<220> <223> PLORF32M-14-5.pep

<400> 207

Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys
1 5 10 15

Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys 20 25 30

Pro	Arg	His 35	Arg	Pro	Ala	Ser	Arg 40	Leu	Ala	Ala	Val	Val 45	Gly	Gly	Val
Ala	Ala 50	Val	Pro	Ala	Val	Val 55	Ser	Gly	Val	Thr	Gly 60	Leu	Ile	Leu	Ser
Pro 65	Ser	Pro	Ser	Pro	Ile 70	Phe	Ile	Gln	Pro	Thr 75	Pro	Ser	Pro	Pro	Met 80
Ser	Phe	His	Asn	Pro 85	Gly	Leu	Glu	Leu	Ala 90	Leu	Asp	Ser	Arg	Pro 95	Ala
Pro	Leu	Ala	Pro 100	Leu	Gly	Val	Thr	Ser 105	Pro	Ser	Ala	Pro	Pro 110	Leu	Pro
Pro	Val	Val 115	Asp	Leu	Pro	Gln	Leu 120	Gly	Leu	Arg	Arg	Gly 125	Ala	Asp	Gly
Thr	Ala 130	Glu	Leu	Thr	Thr	Thr 135	Ala	Ala	Thr	Arg	Phe 140	Met	Lys	Asp	Leu
His 145	Phe	Ala	Gly	Thr	Asn 150	Gly	Val	Gly	Glu	Val 155	Gly	Arg	Gly	Ile	Ala 160
Leu	Thr	Leu	Phe	Asn 165	Leu	Ala	Asp	Thr	Leu 170	Leu	Gly	Gly	Leu	Pro 175	Thr
Glu	Leu	Ile	Ser 180	Ser	Ala	Gly	Gly	Gln 185	Leu	Phe	Tyr	Ser	Arg 190	Pro	Val
Val	Ser	Ala 195	Asn	Gly	Glu	Pro	Thr 200	Val	Lys	Leu	Tyr	Thr 205	Ser	Val	Glu
Asn	Ala 210	Gln	Gln	Asp	Lys	Gly 215	Ile	Thr	Ile	Pro	His 220	Asp	Ile	Asp	Leu
Gly 225	Asp	Ser	Arg	Val	Val 230	Ile	Gln	Asp	Tyr	Asp 235	Asn	Gln	His	Glu	Gln 240
Asp	Arg	Pro	Thr	Pro 245	Ser	Pro	Ala	Pro	Ser 250	Arg	Pro	Phe	Ser	Val 255	Leu
Arg	Ala	Asn	Asp 260	Val	Leu	Trp	Leu	Ser 265	Leu	Thr	Ala	Ala	Glu 270	Tyr	Asp
Gln	Thr	Thr 275	Tyr	Gly	Ser	Ser	Thr 280	Asn	Pro	Met	Tyr	Val 285	Ser	Asp	Thr
Val	Thr 290	Leu	Val	Asn	Val	Ala 295	Thr	Gly	Ala	Gln	Ala 300	Val	Ala	Arg	Ser
Leu 305	Asp	Trp	Ser	Lys	Val 310	Thr	Leu	Asp	Gly	Arg 315	Pro	Leu	Thr	Thr	Ile 320
Gln	Gln	Tyr	Ser	Lys 325	Thr	Phe	Tyr	Val	Leu 330	Pro	Leu	Arg	Gly	Lys 335	Leu

Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr 340 345 350	
Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His 355 360 365	
Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro Thr 370 375 380	
Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Val 385 390 395 400	
Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp 405 410 415	
Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln 420 425 430	
Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr 435 440 445	
Arg Glu Ser Asp Tyr Lys Asp Asp Asp Lys 450 455	
<210> 208 <211> 36 <212> DNA <213> Hepatitis E virus  <220> <223> Description of Artificial Sequence: Primer orf2mid5p	
<400> 208 tatatgaatt catgggtgct gatgggactg ctgagc	36
<210> 209 <211> 418 <212> DNA <213> Hepatitis E virus	
<220> <223> 1440ol.seq	
<220> <221> CDS <222> (3)(416)	
<pre>&lt;400&gt; 209 ct ggc aty act act gcy att gag cag gct gct ctg gct gcg gcc aat    Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn</pre>	47
tee gee ttg geg aat get gtg gtg gtt egg eeg ttt tta tee egt gtt	95

Ser Ala Leu	Ala Asn	Ala Va	l Val	Val	Arg 25	Pro	Phe	Leu	Ser	Arg 30	Val	
caa act gat Gln Thr Asp			_	_			_	_				143
cgg cct gaa Arg Pro Glu 50	_			_		_	_	_				191
gag ctg gaa Glu Leu Glu 65			g Āla	_	-		_	_				239
ggc gct cac Gly Ala His 80				_				_	_			287
tgc ttt ctc Cys Phe Leu												335
ccc act cgt Pro Thr Arg				_	_	_				-		383
ttg ccc cct Leu Pro Pro 130	-	_		_		_	aa					418
<210> 210 <211> 138 <212> PRT <213> Hepat	itis E v	irus										
<400> 210 Gly Xaa Thr 1	Thr Xaa 5	Ile Gl	ı Gln	Ala	Ala 10	Leu	Ala	Ala	Ala	Asn 15	Ser	
Ala Leu Ala	Asn Ala 20	Val Va	l Val	Arg 25	Pro	Phe	Leu	Ser	Arg 30	Val	Gln	
Thr Asp Ile	Leu Ile	Asn Le	ı Met 40	Gln	Pro	Arg	Gln	Leu 45	Val	Phe	Arg	
Pro Glu Val 50	Leu Trp	Asn Hi		Ile	Gln	Arg	Val 60	Ile	His	Asn	Glu	
Leu Glu Gln 65	Tyr Cys	Arg Ala	a Arg	Ala	Gly	Arg 75	Cys	Leu	Glu	Val	Gly 80	
Ala His Pro	Arg Ser 85	Ile As	n Asp	Asn	Pro 90	Asn	Val	Leu	His	Arg 95	Cys	

35

#### 118/140

100 105 110 Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu 120 Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp 135 <210> 211 <211> 197 <212> DNA <213> Hepatitis E virus <220> <223> 1440o2.seq <220> <221> CDS <222> (2)..(196) <400> 211 g aca gaa ttr att tcg tcg gct gga ggt caa ctg ttc tac tcc cgc ccg 49 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro gtt gtc tca gcc aat ggc gag ccg act gtt aag tta tac acc tct gtc Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val 25 gag aat gca cag cag gat aag ggc att gct ata cca cat gat ata gac Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp tta ggg gat tcc cgt gtg gtt ata caa gat tat gay aac car cay gaa 193 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Glu 55 60 caa g 197 Gln 65 <210> 212 <211> 65 <212> PRT <213> Hepatitis E virus <400> 212 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val 20 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp

40

Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu 50 55 60	
Gln 65	
<210> 213 <211> 418 <212> DNA <213> Hepatitis E virus	
<220> <223> 2015-1.seq	
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<pre>&lt;400&gt; 213 ct ggc aty act act gcy att gag cag gct gct ctg gct gcg gct aac    Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn</pre>	47
tct gcc ttg gcg aat gct gtg gtg gtc cgg ccg ttc ctg tcc cgc act Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Thr . 20 25 30	95
cag act gat att ctt att aat ttg atg caa ccc cgg caa ctt gta ttc Gln Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe 35 40 45	143
cgc cct gag gtt ttg tgg aac cat ccg atc cag cga gtc ata cat aat Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn 50 55 60	191
gag ctg gag cag tat tgc cgt gct cgt gct ggt cgc tgc ctg gag gtt Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val 65 70 75	239
ggg gct cat cca aga tct atc aat gac aac cct aat gtt ctg cac cgg Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg 80 85 90 95	287
tgt ttc ctc cgt ccg gtt ggg cga gac gta cag cgt tgg tat tct gcc Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala 100 105 110	335
cct act cgc ggc ccg gcg gct aat tgc cgc cgt tcc gcg tta cgt ggc Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly 115 120 125	383
cta cct cct gtc gac cgc act tac tgt yty gat gg Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp 130 135	418

<210> 214 <211> 138 <212> PRT	
<213> Hepatitis E virus	
<pre>&lt;400&gt; 214 Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser 1 5 10 15</pre>	
Ala Leu Ala Asn Ala Val Val Val Pro Phe Leu Ser Arg Thr Gln 20 25 30	
Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg 35 40 45	
Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu 50 55 60	
Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly 65 70 75 80	
Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys 85 90 95	
Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro 100 105 110	
Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu 115 120 125	
Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp 130 135	
<210> 215 <211> 197 <212> DNA <213> Hepatitis E virus	
<220> <223> 201502.seq	
<220> <221> CDS <222> (2)(196)	
<pre>&lt;400&gt; 215 g aca gaa ttr att tcg tcg gct gga ggc cag ctc ttc tac tcc cgc cca 4 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro 1 5 10 15</pre>	<u> </u>
gtc gtc tca gcc aat ggc gag ccg act gtt aaa ttg tat aca tcc gtc Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val 20 25 30	) 7
gag aat geg cag cag gag aag gge att geg ata eea cat gat ata gat 1	,

Glu Asn Ala Gln Gln Asp Lys Gly Ile Al 35 40	a Ile Pro His Asp Ile Asp 45
cta gga gat tcc cgc gtg gtt atc cag ga Leu Gly Asp Ser Arg Val Val Ile Gln As 50 55	
caa g Gln 65	<b>197</b>
<210> 216 <211> 65 <212> PRT <213> Hepatitis E virus	
<400> 216 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gl 1 5 1	n Leu Phe Tyr Ser Arg Pro 0 15
Val Val Ser Ala Asn Gly Glu Pro Thr Va	l Lys Leu Tyr Thr Ser Val 30
Glu Asn Ala Gln Gln Asp Lys Gly Ile Al 35 40	a Ile Pro His Asp Ile Asp 45
Leu Gly Asp Ser Arg Val Val Ile Gln As 50 55	p Tyr Xaa Asn Xaa Xaa Glu 60
Gln 65	
<210> 217 <211> 251 <212> DNA <213> Hepatitis E virus	
<220> <223> 14404-2.seq	
<220> <221> CDS <222> (3)(251) <223> orf2	
<220> <223> orf3 from position 1 to position	165
<pre>&lt;400&gt; 217 at att cat cca acc aac ccc ttt gcc tcc    Ile His Pro Thr Asn Pro Phe Ala Ser</pre>	
ggg gct gga gct cgc cct cga cag ccg gc Gly Ala Gly Ala Arg Pro Arg Gln Pro Al	

30 20 25 tgg cgt gac cag tcc cag cgc ccc ccc gct gtc ccc cgt cgt cga tct Trp Arg Asp Gln Ser Gln Arg Pro Pro Ala Val Pro Arg Arg Ser 35 acc cca act ggg gct gcg ccg cta act gct gtt tca cca gcg cct gat 191 Thr Pro Thr Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp acg gcc cca gtc cct gat gtt gac tct cgt ggc gct atc ttg cgc cgg 239 Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg 251 cag tat aac cta Gln Tyr Asn Leu <210> 218 <211> 83 <212> PRT <213> Hepatitis E virus <400> 218 Ile His Pro Thr Asn Pro Phe Ala Ser Asp Val Val Ser Gln Ser Gly Ala Gly Ala Arg Pro Arg Gln Pro Ala Arg Pro Leu Gly Ser Ser Trp Arg Asp Gln Ser Gln Arg Pro Pro Ala Val Pro Arg Arg Ser Thr 40 Pro Thr Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp Thr 55 Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln 70 75 Tyr Asn Leu <210> 219 <211> 55 <212> PRT <213> Hepatitis E virus <220> <223> 14404-2.seq orf3 <400> 219 Ile Phe Ile Gln Pro Thr Pro Leu Pro Pro Thr Ser Tyr Arg Asn Pro 10 Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Ser Ala Pro Leu

<400> 221

## 123/140

30

25

20

Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Ser Pro Val Val Asp Leu 40 Pro Gln Leu Gly Leu Arg Arg <210> 220 <211> 251 <212> DNA <213> Hepatitis E virus <220> <223> 20154-2.seq <220> <221> CDS <222> (3)..(251) <223> orf2 <220> <223> orf3 from position 1 to position 165 <400> 220 at att cat cca acc aac ccc ttt gcc gcc gac gtc gta tca caa ccc 47 Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser Gln Pro 95 ggg get gga get ege eet ega eag eeg eee ege eee ete gge tee tet Gly Ala Gly Ala Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly Ser Ser 143 tgg cgt gat cag tee cag cge eee tee get gee eee cgt cgt ega tet Trp Arg Asp Gln Ser Gln Arg Pro Ser Ala Ala Pro Arg Arg Ser 40 ace cea get ggg get geg eeg tta act get gtt tee eet geg eee gat 191 Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp 55 acg gee eea gte eee gae gtt gat tee egt ggt gee ate etg ege egg 239 Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg 70 cag tat aac cta 251 Gln Tyr Asn Leu <210> 221 <211> 83 <212> PRT <213> Hepatitis E virus

Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser Gln Pro Gly
1 5 10 15

Ala Gly Ala Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly Ser Ser Trp
20 25 30

Arg Asp Gln Ser Gln Arg Pro Ser Ala Ala Pro Arg Arg Ser Thr
35 40 45

Pro Ala Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp Thr 50 55 60

Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln 65 70 75 80

Tyr Asn Leu

<210> 222

<211> 55

<212> PRT

<213> Hepatitis E virus

<220>

<223> 20154-2.seq orf3

<400> 222

Ile Phe Ile Gln Pro Thr Pro Leu Pro Pro Thr Ser Tyr His Asn Pro 1 5 10 15

Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Ser Ala Pro Leu
20 25 30

Gly Val Ile Ser Pro Ser Ala Pro Pro Leu Pro Pro Val Val Asp Leu
35 40 45

Pro Gln Leu Gly Leu Arg Arg 50 55

<210> 223

<211> 48

<212> PRT

<213> Hepatitis E virus

<220>

<223> US-2 3-2e

<400> 223

Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro 1 5 10 15

Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile
20 25 30

Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Ser

40

<210> 224

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450

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<211> 33
<212> PRT
<213> Hepatitis E virus
<220>
<223> US-2 4-2
<400> 224
Asp Ser Arg Pro Ala Pro Leu Val Pro Leu Gly Val Thr Ser Pro Ser
Ala Pro Pro Leu Pro Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg
             20
Arg
<210> 225
<211> 450
<212> DNA
<213> Hepatitis E virus
<220>
<223> 5p.pile {hpesvp}
<400> 225
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ggcgaatgct gtggtagtta ggccttttct ctctcaccag cagattgaga tcctcattaa 120
cctaatgcaa cctcgccagc ttgttttccg ccccgaggtt ttctggaatc atcccatcca 180
gcgtgtcatc cataacgagc tggagcttta ctgccgcgcc cgctccggcc gctgtcttga 240
aattggcgcc catccccgct caataaatga taatcctaat gtggtccacc gctgcttcct 300
ccgccctgtt gggcgtgatg ttcagcgctg gtatactgct cccactcgcg ggccggctgc 360
taattgeegg egtteegege tgegeggget teeegetget gaeegeaett aetgeetega 420
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<210> 226
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cgggttttct ggctgtaact ttcccgccga

<220>

<sup>&</sup>lt;211> 450

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Hepatitis E virus

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tgcgaatgct gtggtagtta ggccttttct ctctcaccag cagattgaga tccttattaa 120
cctaatgcaa cctcgccagc ttgttttccg ccccgaggtt ttctggaacc accccatcca 180
gegtgteate cataatgage tggagettta etgtegegee egeteeggee getgeettga 240
aattggtgcc cacceteget caataaacga caatcetaat gtggtccacc getgetteet 300
cegecetgee gggegtgatg tteagegttg gtatactget cetaceegeg ggeeggetge 360
taattgeegg ggtteegeac tgegeggget eeeegetget gaeegeactt aetgettega 420
cgggttttct ggctgtaact ttcccgccga
                                                                   450
<210> 227
<211> 450
<212> DNA
<213> Hepatitis E virus
<220>
<223> 5p.pile {hpea}
<400> 227
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tgcgaatgct gtggtagtta ggccttttct ctctcaccag cagattgaga tccttattaa 120
cctaatgcaa cctcgccagc ttgttttccg ccccgaggtt ttctggaacc atcccatcca 180
gcgtgttatc cataatgagc tggagcttta ctgtcgcgcc cgctccggcc gctgcctcga 240
aattggtgcc caccccgct caataaatga caatcctaat gtggtccacc gttgcttcct 300
ccgtcctgcc gggcgtgatg ttcagcgttg gtatactgcc cctacccgcg ggccggctgc 360
taattgccgg cgttccgcgc tgcgcgggct ccccgctgct gaccgcactt actgcttcga 420
cgggttttct ggctgtaact ttcccgccga
                                                                   450
<210> 228
<211> 446
<212> DNA
<213> Hepatitis E virus
<220>
<223> 5p.pile {840455p}
<400> 228
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aatgctgtgg tggttcggcc gttttatct cgcgtgcaaa ccgagattct tattaatttg 120
atgcaacccc ggcagttggt tttccgccct gaggtacttt ggaatcaccc tatccagcgg 180
gttatacata atgaattaga acagtactgc cgggctcggg ctggtcgttg cttggaggtt 240
ggagctcacc caagatccat taatgacaac cccaacgttc tgcatcggtg tttccttaga 300
ccggttggcc gagatgttca gcgctggtac tctgcccca cccgcggccc tgcggctaat 360
tgccgccgct ccgcgttgcg tggtctcccc cccgctgacc gcacttactg ctttgatgga 420
ttctcccgtt gtgcttttgc tgcaga 446

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<211> 450
<212> DNA
<213> Hepatitis E virus

<220>
<223> 5p.pile {hpenssp}

<400> 229
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tgcgaatgct gtggtggtcc ggcctttcct ttcccatcag caggttgaga tccttataaa 120
tctcatgcaa cctcggcagc tggtgtttcg tcctgaggtt ttttggaatc acccgattca 180
acgtgttata cataatgagc ttgagcagta ttgccgtgct cgctcgggtc gctgccttga 240
gattggagcc cacccacgct ccattaatga taatcctaat gtcctccatc gctgcttct 300
ccaccccgtc ggccgggatg ttcagcgctg gtacacagcc ccgactaggg gacctgcggc 360
gaactgtcgc cgctcggcac ttcgtggtct gccaccagcc gaccgcactt actgttttga 420
tggctttgcc ggctgcgtt ttgccgcga
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<211> 450
<212> DNA
<213> Hepatitis E virus
<220>
<223> 5p Consensus
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<220>

<221> variation <222> ()..(450)

<223> The nucleotide identity of each n is indicated in Figure 9.

<400> 230

<210> 230

<210> 229

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nntnatqcaa ceneqneaqn tnqtnttneg neengaggtn ntntggaane aneenatnea 180
ncgngtnatn cataangann tngancnnta ntgncgngcn cgnncnggnc gntgnntnga 240
nnttggngen cancenngnt enatnaanga naancenaan gtnntneane gntgnttnet 300
nnnneengnn ggnegngatg tteagegntg gtannengen cenaenngng gneengenge 360
naantqncqn ngntcngcnn tncgnggnct nccnncngcn gaccgcactt actgnntnga 420
                                                                  450
nggnttnncn ngntgnnnnt ttncngcnga
<210> 231
<211> 300
<212> DNA
<213> Hepatitis E virus
<220>
<223> 3p.pile {hpea} shown in Figure 9B
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ataacatgtc ttttgctgcg cccatgggtt cgcgaccatg cgccctcggc ctattttgct 120
gttgctcctc atgtttctgc ctatgctgcc cgcgccaccg cccggtcagc cgtctggccg 180
ccgtcgtggg cggcgcagcg gcggttccgg cggtggtttc tggggtgacc gggttgattc 240
tragerette graateret atatteater aarraarer ttegereeg atgtearege 300
<210> 232
<211> 300
<212> DNA
<213> Hepatitis E virus
<220>
<223> 3p.pile {hpeuigh} shown in Figure 9B
actgagtcgg tgaagccagt gctcgacttg acaaattcaa tcctgtgtcg ggtggaatga 60
ataacatgtc ttttgctgcg cccatgggtt ggcgaccatg cgccctcggc ctattttgct 120
gttgeteete atgtttetge etategtgee egegeeaceg eeeggteage egtetggeeg 180
ccgtcgtggg cggcgcagcg gcggttccgg cggtggtttc tggggtgacc gggttgattc 240
teageeette geaateeeet atatteatee aaceaaceee ttegeeeceg atgteacege 300
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<211> 300
<212> DNA
<213> Hepatitis E virus
<220>
<223> 3p.pile {hpesvp} shown in Figure 9B
<400> 233
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ataacatgtc ttttgctgcg cccatgggtt cgcgaccatg cgccctcggc ctattttgtt 120
getgeteete atgtttttge etatgetgee egegeeaeeg eeeggteage egtetggeeg 180
ccgtcgtggg cggcgcagcg gcggttccgg cggtggtttc tggggtgacc gggttgattc 240
tragerette graatreest atatteater aarraareer ttegereerg atgtearege 300
<210> 234
<211> 300
<212> DNA
<213> Hepatitis E virus
<220>
<223> 3p.pile {hpenssp} shown in Figure 9B
<400> 234
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ataacatgtg gtttgctgcg cccatgggtt cgccaccatg cgccctaggc ctcttttgct 120
gttgtteete ttgtttetge etatgttgee egegeeaceg aceggteage egtetggeeg 180
ccgtcgtggg cggcgcagcg gcggtaccgg cggtggtttc tggggtgacc gggttgattc 240
teagecette geaateeeet atatteatee aaceaacee tttgeeceag aegttgeege 300
<210> 235
<211> 297
<212> DNA
<213> Hepatitis E virus
<220>
<223> 3p.pile {840453p} shown in Figure 9B
<400> 235
acagagacta tiaaacctgt acttgatete acaaatteea teatacageg ggtggaatga 60
ataacatgtc ttttgcatcg cccatgggat caccatgcgc cctagggctg ttctgttgtt 120
gttcctcatg tttctgccta tgctgcccgc gccaccggcc ggtcagccgt ctggccgtcg 180
ccgtgggcgg cgcagcggcg gtgccggcgg tggtttctgg agtgacaggg ttgattctca 240
gcccttcgcc ctcccctata ttcatccaac caaccccttc gccgccgatg tcgtttc
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<210> 236
<211> 300
<212> DNA
<213> Hepatitis E virus
<220>
<223> 3p Consensus shown in Figure 9B
<220>
<221> variation
<222> (1)..(300)
<223> The nucleotide identity of each n is indicated in
      Figure 9B
<400> 236
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ataacatgtn ntttgenneg eccatgggnt nnnnaecatg egeeetnggn etnttntgnt 120
gntgntcctc ntgtttntgc ctatnntgcc cgcgccaccg nccggtcagc cgtctggccg 180
negnegtggg eggegeageg geggtneegg eggtggttte tggngtgaen gggttgatte 240
teageeette gennteeeet atatteatee aaceaaceee ttngeeneng angtnnnnne 300
<210> 237
<211> 250
<212> DNA
<213> Hepatitis E virus
<223> 3p.pile {hpea} shown in Figure 9C
<400> 237
agegettace etgtttaace ttgetgacae eetgettgge ggtetacega cagaattgat 60
ttegtegget ggtggeeage tgttetaete tegeeeegte gteteageea atggegagee 120
gactgttaag ctgtatacat ctgtggagaa tgctcagcag gataagggta ttgcaatccc 180
gcatgacatc gacctcgggg aatcccgtgt agttattcag gattatgaca accaacatga 240
gcaggaccga
                                                                   250
<210> 238
<211> 250
<212> DNA
<213> Hepatitis E virus
<220>
<223> 3p.pile {hpeuigh} shown in Figure 9C
<400> 238
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agegettace etgtttaace ttgetgacae eetgettgge ggtetacega cagaattgat 60 ttegtegget ggtggceage tgttetaete tegeceegte gteteageea atggegagee 120 gactgttaag ctgtatacat ctgtagagaa tgctcagcag gataagggta ttgcaatccc 180 gcatgacatc gacctcgggg aatctcgagt tgttattcag gattatgaca accaacatga 240 gcaggaccgg 250 <210> 239 <211> 250 <212> DNA <213> Hepatitis E virus <220> <223> 3p.pile {hpesvp} shown in Figure 9C <400> 239 agccctcacc ctgttcaacc ttgctgacac tctgcttggc ggcctgccga cagaattgat 60 ttegtegget ggtggeeage tgttetaete eegteeegtt gteteageea atggegagee 120 gactgttaag ttgtatacat ctgtagagaa tgctcagcag gataagggta ttgcaatccc 180 gcatgacatt gacctcggag aatctcgtgt ggttattcag gattatgata accaacatga 240 250 acaagatcgg <210> 240 <211> 250 <212> DNA <213> Hepatitis E virus <220> <223> 3p.pile {hpenssp} shown in Figure 9C <400> 240 agetetaaca ttaettaace ttgetgacae geteetegge gggeteeega cagaattaat 60 ttegtegget ggegggeaac tgttttatte eegeeeggtt gteteageea atggegagee 120 aaccgtgaag ctctatacat cagtggagaa tgctcagcag gataagggtg ttgctatccc 180 ccacgatatc gatcttggtg attcgcgtgt ggtcattcag gattatgaca accagcatga 240 250 gcaggatcgg <210> 241 <211> 250 <212> DNA

<sup>&</sup>lt;213> Hepatitis E virus

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<223> 3p.pile {840453p} shown in Figure 9C
<400> 241
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ttegtegget gggggteaac tgttttaete eegeeetgtt eagaattgat ttegtegget 120
gggggtcaac tgttttactc ccgccctgtt tgcgcagcaa gacaagggca tcaccattcc 180
acacgacata gatttaggtg actcccgtgt ggttatccag gattatgata accagcacga 240
                                                                   250
acaagatcga
<210> 242
<211> 250
<212> DNA
<213> Hepatitis E virus
<220>
<223> 3p Consensus shown in Figure 9C
<220>
<221> variation
<222> ()..(250)
<223> The nucleotide identity of each n is indicated in
      Figure 9C
<400> 242
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ttegtegget ggnggneane tgttntante negneengtn gtetengeea atggegagee 120
nacngtnaag ntntanacat engtngagaa tgeneagean ganaagggnn tnnenatnee 180
ncanganatn ganntnggng antcncgngt ngtnatncag gattatgana accancanga 240
ncangancgn
                                                                   250
<210> 243
<211> 418
<212> DNA
<213> Hepatitis E virus
<223> Aulol-wlabolpl.pat
<220>
<221> CDS
<222> (3)..(416)
<400> 243
ct ggc aty act act gcy att gag caa gct gct ctg gct gcg gcc aat
                                                                   47
  Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Asn
                                        10
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						gtg Val										95
_						aac Asn	_	_				_	_			143
						aat Asn										191
		_			_	cgg Arg 70	_		_		_	_				239
	_					att Ile		-				_	_			287
-		_	_	_	-	gly aaa		_	_	_						335
		_			-	gct Ala										383
			_	_	_	act Thr		_		_	aa					418
<211 <212	)> 24 L> 13 2> PF 3> He	88 ?T	tis	E vi	.rus											
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Ala	Leu	Ala	Asn 20	Ala	Val	Val	Val	Arg 25	Pro	Phe	Leu	Ser	Arg 30	Val	Gln	
Thr	Glu	Ile 35	Leu	Ile	Asn	Leu	Met 40	Gln	Pro	Arg	Gln	Leu 45	Val	Phe	Arg	
Pro	Glu 50	Val	Leu	Trp	Asn	His 55	Pro	Ile	Gln	Arg	Val 60	Ile	His	Asn	Glu	
Leu 65	Glu	Gln	Tyr	Cys	Arg 70	Ala	Arg	Ala	Gly	Arg 75	Cys	Leu	Glu	Val	Gly 80	
Ala	His	Pro	Arg	Ser 85	Ile	Asn	Asp	Asn	Pro 90	Asn	Val	Leu	His	Arg 95	Cys	

Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro 105 100 Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu 115 120 Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp 135 <210> 245 <211> 197 <212> DNA <213> Hepatitis E virus <220> <223> Aulo2-wlao2.pat <220> <221> CDS <222> (2)..(196) <400> 245 g aca gaa ttr att tcg tcg gct ggg gga cag tta ttc tac tcc cgc cct 49 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro gty gtc tca gcc aat ggc gag ccg act gtt aaa tta tat aca tct gta 97 Xaa Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val 20 gag aat gcg cag cag gac aag ggg att gcc atc cca cat gat ata gat 145 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp 45 35 ctg ggc gac tct cgt gtg gtg atc cag gat tat gay aac car cay gaa 193 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu 50 55 197 caa g Gln 65 <210> 246 <211> 65 <212> PRT <213> Hepatitis E virus <400> 246 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro 15 Xaa Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val

Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp

35 40 45 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu 55 Gln 65 <210> 247 <211> 418 <212> DNA <213> Hepatitis E virus <220> <223> Arlol- f73olpl.pat <220> <221> CDS <222> (3)..(416) <400> 247 ct ggc aty act act gcy att gag caa gct gct ctg gct gcg gcc aac 47 Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Asn tet gee ttg geg aat get gtg gtt egg eeg ttt tta tee egt gtg 95 Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val cag acc gag att ctt att aac cta atg caa ccc cgg cag ctg gtt ttt 143 Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe cgt cct gag gtg ctt tgg aac cat cct atc cag cgg gtt att cat aat 191 Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn gag tta gaa cag tac tgt cgg gct cgg gct ggt cgc tgc cta gag gtc 239 Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val ggg gcc cac cca agg tcc att aat gat aac cct aat gtt ttg cac cgg 287 Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg 85 90 tgc ttc cta cga cca gtc ggg agg gat gtt caa cgt tgg tat tcc gcc 335 Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala ccc acc cgc ggt cct gct gcc aac tgc cgc cgt tcc gct ctg cgc ggc 383 Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly ctc cct ccc gtc gac cgc act tac tgt yty gat gg 418

Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp

135

130

<210> 248 <211> 138

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	)> 24 Xaa		Thr	Xaa 5	Ile	Glu	Gln	Ala	Ala 10	Leu	Ala	Ala	Ala	Asn 15	Ser	
Ala	Leu	Ala	Asn 20	Ala	Val	Val	Val	Arg 25	Pro	Phe	Leu	Ser	Arg 30	Val	Gln	
Thr	Glu	Ile 35	Leu	Ile	Asn	Leu	Met 40	Gln	Pro	Arg	Gln	Leu 45	Val	Phe	Arg	
Pro	Glu 50	Val	Leu	Trp	Asn	His 55	Pro	Ile	Gln	Arg	Val 60	Ile	His	Asn	Glu	
Leu 65	Glu	Gln	Tyr	Cys	Arg 70	Ala	Arg	Ala	Gly	Arg 75	Cys	Leu	Glu	Val	Gly 80	
Ala	His	Pro	Arg	Ser 85	Ile	Asn	Asp	Asn	Pro 90	Asn	Val	Leu	His	Arg 95	Cys	
Phe	Leu	Arg	Pro 100	Val	Gly	Arg	Asp	Val 105	Gln	Arg	Trp	Tyr	Ser 110	Ala	Pro	
Thr	Arg	Gly 115	Pro	Ala	Aļa	Asn	Cys 120	Arg	Arg	Ser	Ala	Leu 125	Arg	Gly	Leu	
Pro	Pro 130	Val	Asp	Arg	Thr	Tyr 135	Cys	Xaa	Asp							
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	L> CI		(144)	)										,		
gty		tcr		aat Asn 5												48
			_	cag Gln	_		~ ~ ~		_				_		_	96

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Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
20 25 30

Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu 35 40 45

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Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn
1 5 10 15

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cag act gag atc ctt att aac tta atg car ccc cgg car ctg gtt ttc 143 Gln Thr Glu Ile Leu Ile Asn Leu Met Xaa Pro Arg Xaa Leu Val Phe 35 40 45

cgt ccc gag gtg ctt tgg aat cat ccc att caa cgg gtt att cat aat 191 Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn 50 55 60

gaa tta gag cag tac tgc cgg acc cgg gct ggc cgt tgt tta gag gtc 239 Glu Leu Glu Gln Tyr Cys Arg Thr Arg Ala Gly Arg Cys Leu Glu Val 65 70 . 75

gga gcc cat cca agg tcc att aat gac aac cct aac gtt cyg cac cgg 287 Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Xaa His Arg 80 85 90 95

						glà aaa										335
						gct Ala						_	_	_		383
						act Thr					aa					418
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Ala	Leu	Ala	Asn 20	Ala	Val	Val	Val	Arg 25	Pro	Phe	Leu	Ser	Arg 30	Val	Gln	
Thr	Glu	Ile 35	Leu	Ile	Asn	Leu	Met 40	Xaa	Pro	Arg	Xaa	Leu 45	Val	Phe	Arg	
Pro	Glu 50	Val	Leu	Trp	Asn	His 55	Pro	Ile	Gln	Arg	Val 60	Ile	His	Asn	Glu	
Leu 65	Glu	Gln	Tyr	Cys	Arg 70	Thr	Arg	Ala	Gly	Arg 75	Cys	Leu	Glu	Val	Gly 80	
Ala	His	Pro	Arg	Ser 85	Ile	Asn	Asp	Asn	Pro 90	Asn	Val	Xaa	His	Arg 95	Cys	
Phe	Leu	Arg	Pro 100	Val	Gly	Arg	Asp	Val 105	Gln	Arg	Trp	Tyr	Ser 110	Ala	Pro	
Thr	Arg	Gly 115	Pro	Ala	Ala	Asn	Cys 120	Arg	Arg	Ser	Ala	Leu 125	Arg	Gly	Leu	
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gtc Val	gtc Val	tca Ser	gcc Ala 20	aat Asn	ggc Gly	gag Glu	ccg Pro	act Thr 25	gtt Val	aag Lys	ttg Leu	tat Tyr	aca Thr 30	tct Ser	gtg Val	97
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									gat Asp							193
caa Gln 65	_														·	197
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Val	Val	Ser	Ala 20	Asn	Gly	Glu	Pro	Thr 25	Val	Lys	Leu	Tyr	Thr 30	Ser	Val	
Glu	Asn	Ala 35	Gln	Gln	Asp	Lys	Gly 40	Ile	Ala	Ile	Pro	His 45	Asp	Ile	Asp	
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